



SEQUENCE LISTING

<110> Reinherz, Ellis L.
 Freund, Christian
 Li, Jing
 Nishizawa, Kazuhisa
 Wagner, Gerhard

<120> Cloning and Characterization of a CD2
 Binding Protein (CD2BP2)

<130> 1062.1021-004

<140> 09/873,106
<141> 2001-06-01

<150> US 60/111,007
<151> 1998-12-04

<150> US 60/115,647
<151> 1999-01-13

<150> PCT/US99/26993
<151> 1999-11-15

<160> 25

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1299
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (121) ... (1143)

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 a t g c c a a a g g a g g a a a g t g a c c t t c a a g g c g t g g g a g a t g a g g a g g a t 168
 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
 1 5 10 15

g a g g a t g a a a t c a t t g t c c c a a g a a g c t g g a c c t g c t g g c t 216
 Glu Asp Glu Ile Ile Val Pro Lys Lys Leu Val Asp Pro Val Ala
 20 25 30

g g g t c a g g g g t c c t g g g a g c c g c t t t a a a g g c a a a c a c t c t t g g a t 264
 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
 35 40 45

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agc gat gag gag gag gat gat gat gat gat ggg ggg tcc agc aaa tat gac Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp	312
50 55 60	
atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro	360
65 70 75 80	
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85 90 95	
gag gaa ggc cac ttt gat gcc gat ggc aac tac ttc ctg aac cgg gat Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp	456
100 105 110	
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115 120 125	
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130 135 140	
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145 150 155 160	
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165 170 175	
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195 200 205	
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210 215 220	
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225 230 235 240	
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245 250 255	
gag gag gaa ctg gag acc cca acc cct acc cag aga gga gaa gca gag Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu	936
260 265 270	

tcg	cgg	gga	gat	ggt	ctg	gtg	gat	gtg	atg	tgg	gaa	tat	aag	tgg	gag	984	
Ser	Arg	Gly	Asp	Gly	Leu	Val	Asp	Val	Met	Trp	Glu	Tyr	Lys	Trp	Glu		
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aac	acg	ggg	gat	gcc	gag	ctg	tat	ggg	ccc	ttc	acc	agc	gcc	cag	atg	1032	
Asn	Thr	Gly	Asp	Ala	Glu	Leu	Tyr	Gly	Pro	Phe	Thr	Ser	Ala	Gln	Met		
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cag	acc	tgg	gtg	agt	gaa	ggc	tac	ttc	ccg	gac	ggt	gtt	tat	tgc	cgg	1080	
Gln	Thr	Trp	Val	Ser	Glu	Gly	Tyr	Phe	Pro	Asp	Gly	Val	Tyr	Cys	Arg		
305					310					315				320			
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Lys	Leu	Asp	Pro	Pro	Gly	Gly	Gln	Phe	Tyr	Asn	Ser	Lys	Arg	Ile	Asp		
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Phe	Asp	Leu	Tyr	Thr													
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Glu	Glu	Gly	His	Phe	Asp	Ala	Asp	Gly	Asn	Tyr	Phe	Leu	Asn	Arg	Asp		
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							165	170			175						
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							180	185			190						
Pro	Ser	Ser	Pro	Gln	Arg	Leu	Asp	Arg	Leu	Ser	Gly	Leu	Ala	Asp	Gln		
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Met	Val	Ala	Arg	Gly	Asn	Leu	Gly	Val	Tyr	Gln	Glu	Thr	Arg	Glu	Arg		
							210	215			220						

Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
 225 230 235 240
 Asn Pro Thr Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
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 260 265 270
 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
 275 280 285
 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
 290 295 300
 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
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 Phe Asp Leu Tyr Thr
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 <212> PRT
 <213> Homo sapiens

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 <212> PRT
 <213> Caenorhabditis elegans

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<213> Caenorhabditis elegans

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<212> PRT

<213> Saccharomyces cerevisiae

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Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser
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<212> PRT

<213> Saccharomyces cerevisiae

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Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser
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<212> PRT

<213> Artificial Sequence

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<223> Motif in CD2 binding region of CD2BP2

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<222> 1,2,4,5,6,7,9,10,11,12,13,14,15

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 3

<223> Xaa can be Tyr or Phe

<221> VARIANT

<222> 8

<223> Xaa can be Met or Val

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Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Tyr
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Phe

<210> 10
<211> 6
<212> PRT
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<223> CD2BP2 binding region

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<210> 11
<211> 70
<212> PRT
<213> Homo sapiens

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Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro
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50 55 60
Leu Ser Pro Ser Ser Asn
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<212> DNA
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<223> Kozak consensus sequence

<400> 12
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<210> 13
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<220>
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<210> 15
<211> 31
<212> PRT
<213> Gallus gallus

<220>
<223> Flag Epitope

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<213> Drosophila melanogaster

<220>
<223> Flag Epitope

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<210> 17
<211> 34
<212> PRT
<213> Leishmania major

<220>
<223> Flag Epitope

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Lys Lys

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<211> 36
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<213> *Caenorhabditis elegans*

<220>
<223> Flag Epitope

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<210> 19
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<220>
<223> Flag Epitope

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<210> 20
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<213> *Saccharomyces cerevisiae*

<220>
<223> Flag Epitope

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Thr Pro Thr
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<211> 31
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<213> *Saccharomyces pombe*

<220>
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<210> 22
<211> 21
<212> PRT
<213> *Homo sapiens*

<220>
<223> Flag Epitope

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Pro Pro Gly His Arg
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<210> 23
<211> 62
<212> PRT
<213> *Homo sapiens*

<220>
<223> Flag Epitope

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<210> 24
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<212> PRT
<213> *Homo sapiens*

10/10

<220>

<223> Flag Epitope

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<210> 25

<211> 31

<212> PRT

<213> Homo sapiens

<220>

<223> Flag Epitope

<400> 25

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Gln	Glu	Met	Ala	Glu	Trp	Phe	Gln	Ala	Gly	Tyr	Phe	Ser	Met	Ser	
				20				25				30			

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):



- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: Sequences which lack a SEQ ID NO: tag are disclosed on pages 16, 19 and 20 of the specification. See attached Office Action

Applicant Must Provide:ONLY IF THE CRF DOES NOT CONTAIN SAID SEQUENCE.

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

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